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Docket No.: PC-0025 CIP

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

SEP 10 2002

In re Application of: Michael G. Walker

TECH CENTER 1600/2900

Title: ANKYRIN REPEAT DOMAIN 2 PROTEIN VARIANT

Serial No.: 09/758,593

Filing Date: January 10, 2001

Examiner: Holbrook, P

Group Art Unit: 1647

Commissioner for Patents
Washington, D.C. 20231

15/B
M.G.J
9/16/02

RESPONSE TO OFFICE ACTION

Sir:

This paper is responsive to the Office Action dated May 1, 2002, Applicant(s) request reconsideration of the above-referenced patent application in view of the following amendments and remarks. Please note the period for response having been extended until September 1, 2002, by the accompanying Petition and fee.

IN THE SPECIFICATION

Please replace the paragraph beginning at page 29, line 10, with the following rewritten paragraph:

B' The BLAST software suite, freely available sequence comparison algorithms (NCBI, Bethesda MD), includes various sequence analysis programs including "blastn" that is used to align nucleic acid molecules and BLAST 2 that is used for direct pairwise comparison of either nucleic or amino acid molecules. BLAST programs are commonly used with gap and other parameters set to default settings, e.g.: Matrix: BLOSUM62; Reward for match: 1; Penalty for mismatch: -2; Open Gap: 5 and Extension Gap: 2 penalties; Gap x drop-off: 50; Expect: 10; Word Size: 11; and Filter: on. Identity is measured over the entire length of a sequence or some smaller portion thereof. Brenner et al. (1998; Proc Natl Acad Sci